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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/729,571	12/05/2003	Marie Anderson	ASZD-P01-007	8775

44992 7590 12/21/2006
ASTRAZENECA R&D BOSTON
35 GATEHOUSE DRIVE
WALTHAM, MA 02451-1215

EXAMINER

STEADMAN, DAVID J

ART UNIT	PAPER NUMBER
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1656

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
31 DAYS	12/21/2006	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

TH

Office Action Summary

Application No.

10/729,571

Applicant(s)

ANDERSON ET AL.

Examiner

David J. Steadman

Art Unit

1656

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 1 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 16 October 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 8-11 and 48-58 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☐ Claim(s) _____ is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☒ Claim(s) 8-11 and 48-58 are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>See Continuation Sheet</u> . |

Continuation of Attachment(s) 6). Other: CRF Error Report, Notice to Comply.

DETAILED ACTION

Status of the Application

- [1] Claims 8-11 and 48-58 are pending in the application.
- [2] Applicant's amendment to the claims, filed on 16 October 2006, is acknowledged. This listing of the claims replaces all prior versions and listings of the claims in accordance with 37 CFR 1.121(c).
- [3] Applicant's amendment to the specification, filed on 16 October 2006, is acknowledged.
- [4] Receipt of a sequence listing in computer readable form (CRF), a paper copy thereof, a statement of their sameness, a statement that no new matter has been added to the specification by the paper copy of the sequence CRF, and an amendment directing entry of the substitute sequence listing, all filed on 16 October 2006, is acknowledged.

Election/Restrictions

- [5] The examined claims filed on 27 January 2006 are generic with respect to the characteristics of the claimed crystals. This Office action is a supplemental requirement for restriction in view of the instant claims, which recite crystals with specific space groups and unit cell dimensions. See MPEP § 811.02.
- [6] Restriction to one of the following inventions is required under 35 U.S.C. 121:
- I. Claims 8-11, 48-51, 54-55, and 57-58, drawn to crystals of *H. pylori* Murl having space group $P2_1$, classified in class 435, subclass 233.

Art Unit: 1656

- II. Claims 8-11, 52, and 56-58, drawn to crystals of *H. pylori* Murl having space group $P2_12_12_1$, classified in class 435, subclass 233.
- III. Claims 8-11, 53, and 57-58, drawn to crystals of *H. pylori* Murl having space group $P2_12_12$, classified in class 435, subclass 233.

[7] The inventions are distinct, each from the other because:

[8] The crystals of Groups I-III are related as being crystals of *H. pylori* Murl. The related inventions are distinct if the (1) the inventions as claimed are either not capable of use together or can have a materially different design, mode of operation, function, or effect; (2) the inventions do not overlap in scope, i.e., are mutually exclusive; and (3) the inventions as claimed are not obvious variants. See MPEP § 806.05(j). In the instant case, the inventions as claimed have distinct space group symmetries and distinct unit cell dimensions. Furthermore, the inventions as claimed do not encompass overlapping subject matter and there is nothing of record to show them to be obvious variants.

Because these inventions are independent or distinct for the reasons given above and there would be a serious burden on the examiner if restriction is not required because the inventions require a different field of search (see MPEP § 808.02), restriction for examination purposes as indicated is proper.

[9] MPEP § 803 sets forth two criteria for a proper restriction between patentably distinct inventions: (A) The inventions must be independent or distinct as claimed and (B) There must be a serious burden on the examiner. As shown above, the inventions of Groups I-III are independent or distinct, thus satisfying the first criterion for a proper restriction. MPEP § 803 additionally states that a serious burden on the examiner may

Art Unit: 1656

be *prima facie* shown if the examiner shows by appropriate explanation either separate classification, separate status in the art, or a different field of search. In view of the recited limitations of the claims of each invention, a separate patent and non-patent literature search is required. As such, co-examination of the inventions of Groups I-III would require a serious burden on the examiner.

[10] Applicant is advised that the reply to this requirement to be complete must include an election of the invention to be examined even though the requirement be traversed (37 CFR 1.143).

[11] Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

Sequence Compliance

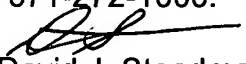
[12] The communication filed on 16 October 2006 is not fully responsive to the Office communication mailed 18 April 2006 for the reason(s) set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements for the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David J. Steadman whose telephone number is 571-272-0942. The examiner can normally be reached on Mon to Fri, 7:30 am to 4:00 pm.

Art Unit: 1656

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr Bragdon can be reached on 571-272-0931. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.



David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656

Notice to Comply	Application No. 10/729,571	Applicant(s) Anderson et al.	
	Examiner Steadman, D.	Art Unit 1656	Paper No 20061214

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or **substitute** computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or **substitute** paper copy of the "Sequence Listing", as well as an amendment directing its entry into the **specification**.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923 .

For CRF Submission Help, call (703) 308-4212 .

Patent Software Program Support

Technical Assistance:.....703-287-0200

To Purchase Patent Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,571C
Source: 1FW/b
Date Processed by STIC: 10/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebs/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/229,571C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

3 <110> APPLICANT: Anderson et al.
 5 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)
 7 <130> FILE REFERENCE: 100966
 9 <140> CURRENT APPLICATION NUMBER: US 10/729,571C
 10 <141> CURRENT FILING DATE: 2003-12-05
 12 <150> PRIOR APPLICATION NUMBER: 60/435,272
 13 <151> PRIOR FILING DATE: 2002-12-20
 15 <150> PRIOR APPLICATION NUMBER: 60/435,167
 16 <151> PRIOR FILING DATE: 2002-12-20
 18 <150> PRIOR APPLICATION NUMBER: 60/435,087
 19 <151> PRIOR FILING DATE: 2002-12-20
 21 <150> PRIOR APPLICATION NUMBER: 60/435,527
 22 <151> PRIOR FILING DATE: 2002-12-20
 E--> 24 <160> NUMBER OF SEQ ID NOS: 76 97 (see p. 22)
 26 <170> SOFTWARE: PatentIn version 3.1

error throughout

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 768
 30 <212> TYPE: DNA
 31 <213> ORGANISM: H. pylori
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(768)

insert
<220>

insert <220>
wherever <221>, <222>, or <223> is shown

<220> is a "header" only. ctk never has a response.

OK-->

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 38 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 39 1 5 10 15
 41 aaa agc ctt tta aaa gcg cga ttg ttt gat gaa atc atc tac tat ggc
 42 Lys Ser Leu Leu Lys Ala Arg Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 43 20 25 30
 45 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag
 46 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 47 35 40 45
 49 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cat gag att gaa
 50 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
 51 50 55 60
 53 tta ttg att gtg gca tgc aac acc gcg agc gct ctg gct tta gaa gag
 54 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 55 65 70 75 80
 57 atg caa aag tat tct aaa atc cct att gtg ggc gtg att gag cca agc
 58 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser

48

96

144

192

240

288

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

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Output Set: N:\CRF4\10202006\J729571C.raw

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62 ile leu ala ile lys arg gln val glu asp lys asn ala pro ile leu
63          100          105          110
65 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gac aac gcc      384
66 val leu gly thr lys ala thr ile gln ser asn ala tyr asp asn ala
67          115          120          125
69 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gct act tct ctt      432
70 leu lys gln gln gly tyr leu asn ile ser his leu ala thr ser leu
71          130          135          140
73 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
74 phe val pro leu ile glu glu ser ile leu glu gly glu leu leu glu
75 145          150          155          160
77 act tgc atg cat tat tat ttc act ccc tta gag att tta ccc gaa gtg      528
78 thr cys met his tyr tyr phe thr pro leu glu ile leu pro glu val
79          165          170          175
81 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
82 ile ile leu gly cys thr his phe pro leu ile ala gln lys ile glu
83          180          185          190
85 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
86 gly tyr phe met gly his phe ala leu pro thr pro pro leu leu ile
87          195          200          205
89 cat tcg ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
90 his ser gly asp ala ile val glu tyr leu gln gln lys tyr ala leu
91          210          215          220
93 aaa aac aat gca tgc aca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
94 lys asn asn ala cys thr phe pro lys val glu phe his ala ser gly
95 225          230          235          240
97 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
98 asp val ile trp leu glu arg gln ala lys glu trp leu lys leu
99          245          250          255
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172 <211> LENGTH: 768
173 <212> TYPE: DNA
174 <213> ORGANISM: H. pylori
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(768)
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182 1          5          10          15
184 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
185 lys ser leu leu lys ala gln leu phe asp glu ile ile tyr tyr gly
186          20          25          30
188 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
189 asp ser ala arg val pro tyr gly thr lys asp pro thr thr ile lys
190          35          40          45
192 caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa      192
193 gln phe gly leu glu ala leu asp phe phe lys pro his gln ile glu

```

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

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Output Set: N:\CRF4\10202006\J729571C.raw

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194      50      55      60
196 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag      240
197 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
198 65      70      75      80
200 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
201 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
202      85      90      95
204 att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta      336
205 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
206      100      105      110
208 gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
209 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
210      115      120      125
212 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
213 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
214      130      135      140
216 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
217 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
218 145      150      155      160
220 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
221 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
222      165      170      175
224 att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag      576
225 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
226      180      185      190
228 ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
229 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
230      195      200      205
232 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt      672
233 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
234      210      215      220
236 aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
237 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
238 225      230      235      240
240 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
241 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
242      245      250      255

```

314 <210> SEQ ID NO: 5

315 <211> LENGTH: 768

316 <212> TYPE: DNA

317 <213> ORGANISM: H. pylori

319 <221> NAME/KEY: CDS

320 <222> LOCATION: (1)..(768)

E--> 322 <400> SEQUENCE: 5

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323 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
324 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
325 1      5      10      15
327 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
328 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

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Insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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329          20          25          30
331 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
332 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
333          35          40          45
335 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
336 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
337          50          55          60
339 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
340 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
341 65          70          75          80
343 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
344 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
345          85          90          95
347 att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta      336
348 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
349          100          105          110
351 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc      384
352 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
353          115          120          125
355 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
356 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
357          130          135          140
359 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
360 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
361 145          150          155          160
363 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg      528
364 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
365          165          170          175
367 att att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
368 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
369          180          185          190
371 ggc tat ttt atg gag cat ttt gcc ctt tca aca ccc ccc cta ctc atc      624
372 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
373          195          200          205
375 cat tcg ggc gat gct att gta gga tat ttg cag caa aaa tac gcc ctt      672
376 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
377          210          215          220
379 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
380 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
381 225          230          235          240
383 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
384 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
385          245          250          255
457 <210> SEQ ID NO: 7
458 <211> LENGTH: 749
459 <212> TYPE: DNA
460 <213> ORGANISM: H. pylori
462 <221> NAME/KEY: CDS
463 <222> LOCATION: (1)..(747)

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insert <220>

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

E--> 465 <400> SEQUENCE: 7

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466 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
467 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
468 1          5          10          15
470 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
471 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
472          20          25          30
474 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
475 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
476          35          40          45
478 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
479 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
480          50          55          60
482 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
483 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
484 65          70          75          80
486 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
487 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
488          85          90          95
490 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta      336
491 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
492          100          105          110
494 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc      384
495 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
496          115          120          125
498 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
499 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
500          130          135          140
502 ttt gtg cct ttg att gaa gaa agt att tta ggg ggc gaa ttg tta gaa      480
503 Phe Val Pro Leu Ile Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu
504 145          150          155          160
506 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
507 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
508          165          170          175
510 att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
511 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
512          180          185          190
514 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
515 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
516          195          200          205
518 cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
519 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
520          210          215          220
522 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
523 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
524 225          230          235          240
526 gat gtg atc tgg cta gaa aaa cag gct aa      749
527 Asp Val Ile Trp Leu Glu Lys Gln Ala
528          245

```

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

600 <210> SEQ ID NO: 9
 601 <211> LENGTH: 768
 602 <212> TYPE: DNA
 603 <213> ORGANISM: H. pylori
 605 <221> NAME/KBY: CDS
 606 <222> LOCATION: (1)..(768) *insert <2207*

E--> 608 <400> SEQUENCE: 9

609	atg	aaa	ata	ggc	gtt	ttt	gat	agc	ggt	gtg	gga	ggg	ttt	agc	ggt	tta	48
610	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
611	1			5					10				15				
613	aaa	agc	ctt	tta	aaa	gcg	caa	cta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
614	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
615				20					25				30				
617	gat	agt	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
618	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
619				35				40				45					
621	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	gga	192
622	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
623				50				55				60					
625	tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gag	240
626	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
627	65				70				75			80					
629	atg	caa	aag	cat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gaa	cca	agc	288
630	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
631				85				90				95					
633	att	tta	gcg	atc	aag	caa	caa	gta	aaa	gat	aaa	aac	gcc	tct	att	ttg	336
634	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Ser	Ile	Leu	
635				100				105				110					
637	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tcc	aac	gct	tat	gac	aac	gcc	384
638	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
639				115				120				125					
641	ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
642	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
643				130				135				140					
645	ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	cta	gaa	480
646	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
647	145				150				155			160					
649	act	tgc	atg	cgt	tat	tat	ttc	act	ccg	tta	gag	atc	ttg	cct	gaa	gtg	528
650	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
651				165				170				175					
653	gtt	att	tta	ggg	tgc	acg	cat	ttt	ccc	tta	atc	gct	caa	aaa	att	gag	576
654	Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
655				180				185				190					
657	ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624
658	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
659				195				200				205					
661	cat	tcg	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
662	His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
663				210				215				220					

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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665 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
666 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
667 225                230                235                240
669 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
670 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
671                245                250                255
743 <210> SEQ ID NO: 11
744 <211> LENGTH: 749
745 <212> TYPE: DNA
746 <213> ORGANISM: H. pylori
748 <221> NAME/KEY: CDS
749 <222> LOCATION: (1)..(747)
E--> 751 <400> SEQUENCE: 11
752 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
753 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
754 1                5                10                15
756 aaa agc ctt tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      96
757 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
758                20                25                30
760 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
761 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
762                35                40                45
764 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
765 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
766                50                55                60
768 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
769 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
770 65                70                75                80
772 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
773 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
774                85                90                95
776 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta      336
777 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
778                100               105               110
780 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
781 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
782                115               120               125
784 cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt      432
785 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
786                130               135               140
788 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
789 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
790 145               150               155               160
792 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
793 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
794                165               170               175
796 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
797 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
798                180               185               190

```

insert <2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

800 ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc      624
801 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
802      195      200      205
804 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt      672
805 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
806      210      215      220
808 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
809 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
810      225      230      235      240
812 gat gtg gtt tgg cta gaa aaa cag gct aa      749
813 Asp Val Val Trp Leu Glu Lys Gln Ala
814      245
886 <210> SEQ ID NO: 13
887 <211> LENGTH: 768
888 <212> TYPE: DNA
889 <213> ORGANISM: H. pylori
891 <221> NAME/KEY: CDS
892 <222> LOCATION: (1)..(768)
E--> 894 <400> SEQUENCE: 13
895 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
896 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
897 1      5      10      15
899 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
900 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
901      20      25      30
903 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
904 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
905      35      40      45
907 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
908 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
909      50      55      60
911 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
912 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
913 65      70      75      80
915 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
916 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
917      85      90      95
919 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
920 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
921      100      105      110
923 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc      384
924 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
925      115      120      125
927 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
928 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
929      130      135      140
931 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
932 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
933 145      150      155      160

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insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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935 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
936 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
937          165          170          175
939 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
940 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
941          180          185          190
943 ggc tat ttt atg gag cat ttt gcc ctt tta acg ccc ccc cta ctc atc      624
944 Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
945          195          200          205
947 cat tct ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
948 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
949          210          215          220
951 aag aaa aat gca cac tca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
952 Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly
953 225          230          235          240
955 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
956 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
957          245          250          255
1029 <210> SEQ ID NO: 15
1030 <211> LENGTH: 768
1031 <212> TYPE: DNA
1032 <213> ORGANISM: H. pylori
1034 <221> NAME/KEY: CDS
1035 <222> LOCATION: (1)..(768)
E--> 1037 <400> SEQUENCE: 15
1038 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1039 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1040 1          5          10          15
1042 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
1043 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
1044          20          25          30
1046 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1047 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1048          35          40          45
1050 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
1051 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
1052          50          55          60
1054 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1055 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1056 65          70          75          80
1058 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc      288
1059 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1060          85          90          95
1062 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
1063 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1064          100          105          110
1066 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc      384
1067 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1068          115          120          125

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Insert <220>

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1070 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1071 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1072      130      135      140
1074 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
1075 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1076 145      150      155      160
1078 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta      528
1079 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
1080      165      170      175
1082 atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag      576
1083 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
1084      180      185      190
1086 ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
1087 Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1088      195      200      205
1090 cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt      672
1091 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
1092      210      215      220
1094 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1095 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1096 225      230      235      240
1098 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1099 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1100      245      250      255
1172 <210> SEQ ID NO: 17
1173 <211> LENGTH: 768
1174 <212> TYPE: DNA
1175 <213> ORGANISM: H. pylori
1177 <221> NAME/KEY: CDS
1178 <222> LOCATION: (1)..(768)
E--> 1180 <400> SEQUENCE: 17
1181 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1182 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1183 1      5      10      15
1185 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1186 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1187      20      25      30
1189 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1190 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1191      35      40      45
1193 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1194 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1195      50      55      60
1197 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag      240
1198 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1199 65      70      75      80
1201 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1202 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1203      85      90      95

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Insert (2207)

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1206 ile leu ala ile lys gln gln val lys asp lys asn ala pro ile leu
1207          100          105          110
1209 gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1210 val leu gly thr lys ala thr ile gln ser asn ala tyr asp asn ala
1211          115          120          125
1213 ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt      432
1214 leu lys arg gln gly tyr leu asn val ser his leu ala thr ser leu
1215          130          135          140
1217 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1218 phe val pro leu ile glu glu ser ile leu glu gly glu leu leu glu
1219 145          150          155          160
1221 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1222 thr cys met arg tyr tyr phe thr pro leu lys ile leu pro glu val
1223          165          170          175
1225 atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag      576
1226 ile ile leu gly cys thr his phe pro leu ile ala gln lys ile glu
1227          180          185          190
1229 ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc      624
1230 gly tyr phe met glu his phe ala phe pro thr pro pro leu leu ile
1231          195          200          205
1233 cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1234 his ser gly asp ala ile val glu tyr leu gln gln lys tyr ala leu
1235          210          215          220
1237 aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc      720
1238 lys lys asn ala his ala leu pro lys val glu phe his ala ser gly
1239 225          230          235          240
1241 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1242 asp val ile trp leu glu lys gln ala lys glu trp leu lys leu
1243          245          250          255
1315 <210> SEQ ID NO: 19
1316 <211> LENGTH: 768
1317 <212> TYPE: DNA
1318 <213> ORGANISM: H. pylori
1320 <221> NAME/KEY: CDS
1321 <222> LOCATION: (1)..(768)
E--> 1323 <400> SEQUENCE: 19
1324 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1325 met lys ile gly val phe asp ser gly val gly gly phe ser val leu
1326 1          5          10          15
1328 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1329 lys ser leu leu lys ala gln leu phe asp glu ile ile tyr tyr gly
1330          20          25          30
1332 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1333 asp ser ala arg val pro tyr gly thr lys asp pro thr thr ile lys
1334          35          40          45
1336 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1337 gln phe gly leu glu ala leu asp phe phe lys pro his gln ile lys
1338          50          55          60

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insert <2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1340 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1341 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1342 65              70              75              80
1344 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1345 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1346              85              90              95
1348 att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta      336
1349 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1350              100             105             110
1352 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1353 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1354              115             120             125
1356 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432
1357 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1358              130             135             140
1360 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa      480
1361 Phe Val Pro Leu Ile Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
1362 145              150             155             160
1364 act tgc atg cgt tat tat ttc act ccc tta gag att tta cct gaa gtg      528
1365 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1366              165             170             175
1368 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
1369 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1370              180             185             190
1372 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc      624
1373 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
1374              195             200             205
1376 cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
1377 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1378              210             215             220
1380 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1381 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1382 225              230             235             240
1384 gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1385 Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1386              245             250             255

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1458 <210> SEQ ID NO: 21

1459 <211> LENGTH: 768

1460 <212> TYPE: DNA

1461 <213> ORGANISM: H. pylori

1463 <221> NAME/KEY: CDS

1464 <222> LOCATION: (1)..(768)

insert C2207

E--> 1466 <400> SEQUENCE: 21

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1467 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1468 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1469 1              5              10              15
1471 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1472 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1473              20              25              30

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RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1475 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1476 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1477      35      40      45
1479 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1480 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1481      50      55      60
1483 tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1484 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1485 65      70      75      80
1487 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1488 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1489      85      90      95
1491 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
1492 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1493      100      105      110
1495 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
1496 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1497      115      120      125
1499 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1500 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1501      130      135      140
1503 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1504 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1505 145      150      155      160
1507 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1508 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
1509      165      170      175
1511 att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
1512 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1513      180      185      190
1515 agc tat ttt atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
1516 Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
1517      195      200      205
1519 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1520 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1521      210      215      220
1523 aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1524 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1525 225      230      235      240
1527 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1528 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1529      245      250      255

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1601 <210> SEQ ID NO: 23

1602 <211> LENGTH: 768

1603 <212> TYPE: DNA

1604 <213> ORGANISM: H. pylori

1607 <221> NAME/KEY: CDS

1608 <222> LOCATION: (1)..(768)

E--> 1610 <400> SEQUENCE: 23

insert (2207)

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1611 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1612 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1613 1          5          10          15
1615 aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc      96
1616 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1617          20          25          30
1619 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1620 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1621          35          40          45
1623 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
1624 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
1625          50          55          60
1627 tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag      240
1628 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1629 65          70          75          80
1631 atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1632 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1633          85          90          95
1635 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta      336
1636 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1637          100          105          110
1639 gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc      384
1640 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1641          115          120          125
1643 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt      432
1644 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
1645          130          135          140
1647 ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1648 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1649 145          150          155          160
1651 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
1652 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1653          165          170          175
1655 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
1656 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1657          180          185          190
1659 agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc      624
1660 Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1661          195          200          205
1663 cat tct ggc gat gct att gtg gaa tac ttg caa caa aaa tac gcc ctt      672
1664 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1665          210          215          220
1667 aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1668 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1669 225          230          235          240
1671 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1672 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1673          245          250          255
1745 <210> SEQ ID NO: 25

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RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1746 <211> LENGTH: 768

1747 <212> TYPE: DNA

1748 <213> ORGANISM: H. pylori

1750 <221> NAME/KEY: CDS

1751 <222> LOCATION: (1)..(768)

E--> 1753 <400> SEQUENCE: 25

insert <2207

1754	atg	aaa	ata	ggc	ggt	ttt	gat	agc	ggg	gtg	gga	ggg	ttt	agc	ggt	tta	48
1755	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1756	1			5					10				15				
1758	aaa	agc	ctt	tta	aaa	gcg	caa	tta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
1759	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
1760				20				25					30				
1762	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
1763	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
1764				35				40					45				
1766	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	aaa	att	gaa	192
1767	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
1768		50				55					60						
1770	tta	tta	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	ctg	gct	tta	gaa	gag	240
1771	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
1772	65				70				75				80				
1774	atg	caa	aag	cat	tcc	aaa	atc	ccc	att	gtg	ggc	gtg	att	gag	cca	agc	288
1775	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
1776				85				90					95				
1778	att	tta	gcg	atc	aaa	caa	caa	gtg	aaa	gat	aaa	aac	acc	cct	att	tta	336
1779	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Thr	Pro	Ile	Leu	
1780				100				105					110				
1782	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tct	aac	gct	tac	gat	aac	gcc	384
1783	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
1784				115				120					125				
1786	ctg	aaa	caa	caa	ggc	tat	ttg	aag	ggt	tcg	cat	ttg	gcc	act	tct	ctt	432
1787	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Lys	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
1788		130				135						140					
1790	ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
1791	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
1792	145				150				155				160				
1794	act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gaa	atc	tta	cct	gaa	gtg	528
1795	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
1796				165				170					175				
1798	ggt	att	tta	ggc	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
1799	Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
1800				180				185					190				
1802	ggc	tat	ttt	atg	gaa	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624
1803	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile	
1804				195				200					205				
1806	cat	tct	ggc	gac	gct	att	gtg	gga	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
1807	His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Lys	Tyr	Ala	Leu		
1808		210				215						220					
1810	aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1811 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1812 225                230                235                240
1814 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1815 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1816                245                250                255
1888 <210> SEQ ID NO: 27
1889 <211> LENGTH: 768
1890 <212> TYPE: DNA
1891 <213> ORGANISM: H. pylori
1893 <221> NAME/KEY: CDS
1894 <222> LOCATION: (1)..(768)
E--> 1896 <400> SEQUENCE: 27
1897 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1898 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1899 1                5                10                15
1901 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
1902 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
1903                20                25                30
1905 gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1906 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1907                35                40                45
1909 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa      192
1910 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
1911                50                55                60
1913 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa      240
1914 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1915 65                70                75                80
1917 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc      288
1918 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1919                85                90                95
1921 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
1922 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1923                100               105               110
1925 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
1926 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1927                115               120               125
1929 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1930 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1931                130               135               140
1933 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
1934 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
1935 145               150               155               160
1937 act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg      528
1938 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1939                165               170               175
1941 gtt att tta ggc tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
1942 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
1943                180               185               190
1945 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624

```

insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1946 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1947          195          200          205
1949 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1950 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1951          210          215          220
1953 aag aaa aac gca tgt gca ttc cct aaa gta gaa ttt cat gcg agc ggc      720
1954 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1955 225          230          235          240
1957 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1958 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1959          245          250          255
2031 <210> SEQ ID NO: 29
2032 <211> LENGTH: 768
2033 <212> TYPE: DNA
2034 <213> ORGANISM: H. pylori
2036 <221> NAME/KEY: CDS
2037 <222> LOCATION: (1)..(768)
E--> 2039 <400> SEQUENCE: 29
2040 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2041 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2042 1          5          10          15
2044 aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc      96
2045 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
2046          20          25          30
2048 gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2049 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2050          35          40          45
2052 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa      192
2053 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
2054          50          55          60
2056 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gga gag      240
2057 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu
2058 65          70          75          80
2060 atg caa aag tat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
2061 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2062          85          90          95
2064 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2065 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2066          100          105          110
2068 gta cta ggg aca aaa gcg acg att cga tcc aac gct tat gac aac gcc      384
2069 Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala
2070          115          120          125
2072 ctg aaa caa caa ggc tat ttg aat att tcg cat tta gcc act tct ctt      432
2073 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
2074          130          135          140
2076 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
2077 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
2078 145          150          155          160
2080 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528

```

insert (2207)

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

2081 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2082                165                170                175
2084 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
2085 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
2086                180                185                190
2088 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2089 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2090                195                200                205
2092 cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac gcc ctt      672
2093 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
2094                210                215                220
2096 aag aaa aac gca tgc gca ttc cct aaa gta gaa ttc cat gcg agc ggc      720
2097 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2098 225                230                235                240
2100 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
2101 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2102                245                250                255
2174 <210> SEQ ID NO: 31
2175 <211> LENGTH: 768
2176 <212> TYPE: DNA
2177 <213> ORGANISM: H. pylori
2179 <221> NAME/KEY: CDS
2180 <222> LOCATION: (1)..(768)
E--> 2182 <400> SEQUENCE: 31
2183 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2184 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2185 1                5                10                15
2187 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
2188 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
2189                20                25                30
2191 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2192 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2193                35                40                45
2195 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
2196 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
2197                50                55                60
2199 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
2200 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
2201 65                70                75                80
2203 atg caa aag cat tcc aaa atc cct att gtg ggt gtg att gag cca agc      288
2204 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2205                85                90                95
2207 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2208 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2209                100                105                110
2211 gtg tta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
2212 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2213                115                120                125
2215 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432

```

insert 2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

2216 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
2217      130                      135                      140
2219 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa      480
2220 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
2221 145                      150                      155                      160
2223 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
2224 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2225                      165                      170                      175
2227 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
2228 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
2229                      180                      185                      190
2231 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc      624
2232 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2233                      195                      200                      205
2235 cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac acc ctt      672
2236 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
2237      210                      215                      220
2239 aag aaa aat gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
2240 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2241 225                      230                      235                      240
2243 gat gtg gtt tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
2244 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2245                      245                      250                      255
2317 <210> SEQ ID NO: 33
2318 <211> LENGTH: 765
2319 <212> TYPE: DNA
2320 <213> ORGANISM: H. pylori
2322 <221> NAME/KEY: CDS
2323 <222> LOCATION: (1)..(765)
E--> 2325 <400> SEQUENCE: 33
2326 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2327 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2328 1                      5                      10                      15
2330 aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc      96
2331 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
2332                      20                      25                      30
2334 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2335 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2336                      35                      40                      45
2338 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
2339 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
2340                      50                      55                      60
2342 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag      240
2343 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
2344 65                      70                      75                      80
2346 atg caa aag cat tcc aaa atc cct gtt gtg ggc gtg att gag cca agc      288
2347 Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser
2348                      85                      90                      95
2350 att tta gcg atc aaa cgg caa gtg aaa gat aaa aac gcc cct att ttg      336

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insert <2207

RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

2351 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2352             100             105             110
2354 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc      384
2355 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2356             115             120             125
2358 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
2359 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
2360             130             135             140
2362 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
2363 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
2364 145             150             155             160
2366 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
2367 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2368             165             170             175
2370 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
2371 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
2372             180             185             190
2374 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2375 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2376             195             200             205
2378 cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt      672
2379 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
2380             210             215             220
2382 aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
2383 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2384 225             230             235             240
2386 gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg      765
2387 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2388             245             250             255

```

3614 <210> SEQ ID NO: 75

3615 <211> LENGTH: 19

3616 <212> TYPE: DNA

3617 <213> ORGANISM: primer

3619 <400> SEQUENCE: 75

E--> 3620 ttatgcaaca aatggacga

19

invalid nucleotide designator

same error in sequence 76

VERIFICATION SUMMARY

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:58

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

L:36 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:179 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:322 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:465 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:608 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
L:751 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:894 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:1037 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:1180 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:1323 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19
L:1466 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:1610 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23
L:1753 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:1896 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:2039 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:2182 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:2325 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33
L:3620 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (76) Counted (97)

10/729,571C

22

<210> 97 last sequence in submitted file
<211> 32
<212> PRT
<213> Enterococcus faecium

<400> 97

Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
1 5 10 15

Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu Ile Asp
20 25 30